

each containing the same number of trials as our recorded data, we found, on average, exactly the abovementioned number of significant tests. This result is consistent with the hypothesis that triplets of each type arise by chance.

Figure 6 illustrates the dangers of multiple comparisons. The top panel shows the number of triplets of each type in the experimental data. The four panels below show the number of triplets of each type in four different sets of data that were simulated using the spike count matched model. These model runs have peaks that are as large as the largest peak found in the data. Thus, although we think that the large peak from the data must be

significant by happens, we must exercise caution because a stochastic model tends to equally large peaks. If we accept the high peaks in the data as significant, we must also accept the high peaks in the simulations as significant, yet we know that the latter were generated by a stochastic process that is directly related to the spike count.

The results show that matching the spike count distribution is critical for matching the numbers of precisely-timed patterns in the data. The reason for this can be seen by examining the relation between the firing rate and the number of repeating triplets. When the firing rate is high, the number of triplets increases very rapidly (Fig. 5C).

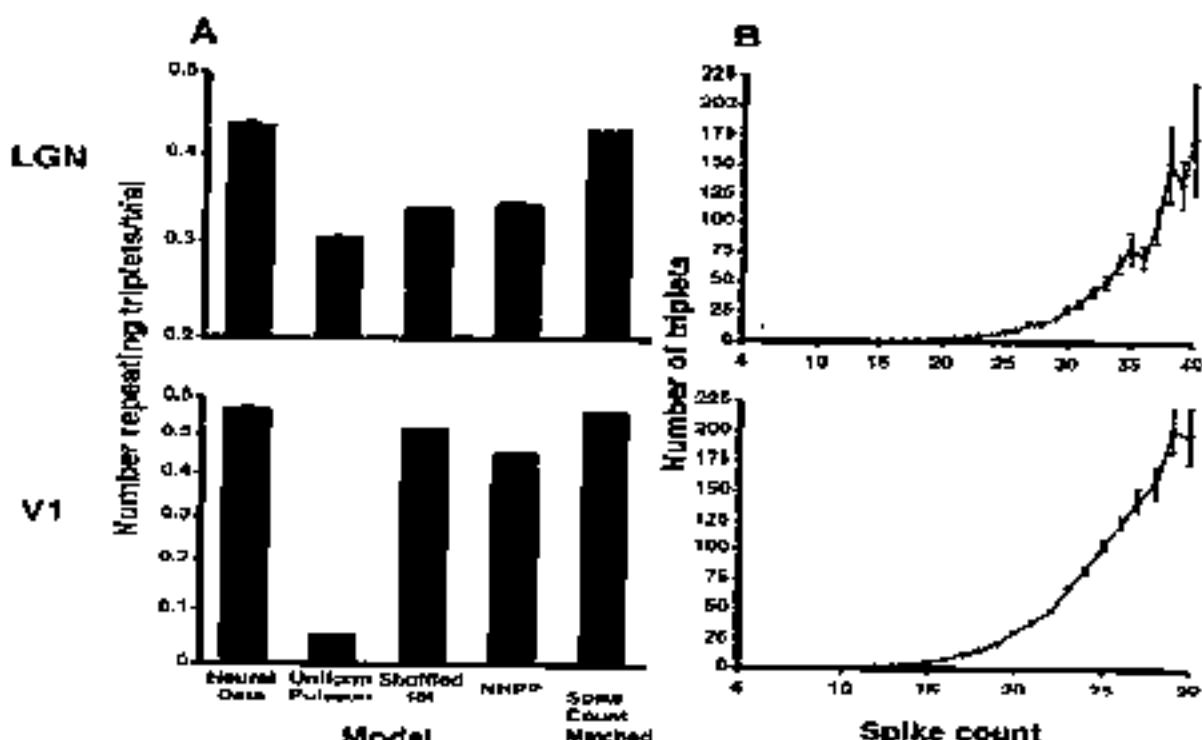


FIG. 5. **A.** The number of repeating triplets seen in the data (left bar) and four models: the uniform Poisson model, the interval shuffling model, the nonhomogeneous Poisson model, and the spike count matched model. The numbers of repeating triplets generated by the spike count matched model are indistinguishable from the number found in the data. The numbers generated by the other 3 models are significantly ($p < 0.001$) different than those found in the data. **B.** Relation of the number of triplets to spike count. The number of triplets increases nonlinearly at all spike counts. If the variability of the response is underestimated the number of triplets predicted will be underestimated because the number of triplets added by a high spike count will not be completely compensated by the number lost at the corresponding low spike count.